



# Sequence Listing

<110> de Sauvage, Frederic J.  
Gurney, Austin  
Murone, Maximilien  
Rosenthal, Arnon  
Stone, Donna M.  
Wood, William I.

<120> Human Suppressor of Fused

<130> P1548R1-US

<140> US 09/581,742

<141> 2000-06-16

<150> US 60/123,090

<151> 1999-03-05

<150> US 60/135,736

<151> 1999-05-25

<150> PCT/US00/05746

<151> 2000-03-02

<160> 10

<210> 1

<211> 1760

<212> DNA

<213> Homo sapiens

<400> 1

cccgcctggcc cgtcagtgct ctccccgtcg ttgcccctct ccagttcccc 50

cagtgccctgc cctacgcacc ccgatggcgg agctgcgggc tagcggcgcc 100

ccccggcccca ccgcgcccc ggccccctggc ccgactgccc ccccggcctt 150

cgttctgctc tttcccccg gactgcacgc catctacgga gagtgccgcc 200

gcctttaccc tgaccagccg aaccgcgtcc aggttaccgc tatcgtcaag 250

tactgggttg gtggcccaga ccccttgac tatgttagca tgtacaggaa 300

tgtggggagc cttctgcta acatccccga gcaactggc tacatcagct 350

tggcctgag tgatctctat ggtgacaaca gagtccatga gtttacagga 400

acagatggac ctagtggttt tggctttgag ttgaccttc gtctgaagag 450

agaaactggg gagtctgcc caccaacatg gccgcagag ttaatgcagg 500

gcttggcacg atacgtgttc cagtcagaga acaccttctg cagtggggac 550

catgtgtcct ggcacagccc ttgggataac agtgagtcaa gaattcagca 600

catgctgctg acagaggacc cacagatgca gcccgctgcag acaccctttg 650  
gggtagttac ctctctccag atcgttggtg tctgcactga agagctacac 700  
tcagcccagc agtggaacgg gcagggcatc ctggagctgc tgcggacagt 750  
gcctattgct ggcggcccct ggctgataac tgacatgcgg aggggagaga 800  
ccatatttga gatcgatcca cacctgcaag agagagttga caaaggcatc 850  
gagacagatg gctccaacct gagtgggtgc agtgccaagt gtgcctggga 900  
tgacctgagc cgcccccccg aggatgacga ggacagccgg agcatctgca 950  
tcggcacaca gccccggcga ctctctggca aagacacaga gcagatccgg 1000  
gagaccctga ggagaggact cgagatcaac agcaaacctg tccttccacc 1050  
aatcaacctt cagcggcaga atggcctcgc ccacgaccgg gccccgagcc 1100  
gcaaagacag cctggaaagt gacagctcca cggccatcat tccccatgag 1150  
ctgattcgca cgcggcagct tgagagcgta catctgaaat tcaaccagga 1200  
gtccggagcc ctcatctctc tctgcctaag gggcaggctc ctgcatggac 1250  
ggcactttac atataaaagt atcacaggtg acatggccat cacgtttgtc 1300  
tccacgggag tggaaggcgc ctttgccact gaggagcatc cttacgcggc 1350  
tcatggaccc tggttacaac tctgaaccta tcctcggagc tctgcctcc 1400  
cgtcctggaa cgtctttctg ccctgaggag agggtagtca gcatctccaa 1450  
ttttcagcag ctcaagaacc ttggccccca caggacttcg cagatgtcac 1500  
attgcccctc agtcccctga atgcccttcg gacccaaccc caattcccca 1550  
agcccctgac cccctagctg ccgggggttc cactcccagt gccacaaccc 1600  
cctcacctcc cctggcagcc cctcagcgag cctgaggccc agcaccgct 1650  
ggctccccag cacatgggtc cctcccatgg gctgttgccc agggaaccgg 1700  
ggcgcggtgg gaacgagctg ctggcctcgg catgtttcaa taaagttgct 1750  
gtgctgggag 1760

<210> 2  
<211> 433  
<212> PRT  
<213> Homo sapien

<400> 2  
Met Ala Glu Leu Arg Pro Ser Gly Ala Pro Gly Pro Thr Ala Pro  
1 5 10 15  
Pro Ala Pro Gly Pro Thr Ala Pro Pro Ala Phe Ala Ser Leu Phe  
20 25 30

Pro	Pro	Gly	Leu	His	Ala	Ile	Tyr	Gly	Glu	Cys	Arg	Arg	Leu	Tyr	35	40	45
Pro	Asp	Gln	Pro	Asn	Pro	Leu	Gln	Val	Thr	Ala	Ile	Val	Lys	Tyr	50	55	60
Trp	Leu	Gly	Gly	Pro	Asp	Pro	Leu	Asp	Tyr	Val	Ser	Met	Tyr	Arg	65	70	75
Asn	Val	Gly	Ser	Pro	Ser	Ala	Asn	Ile	Pro	Glu	His	Trp	His	Tyr	80	85	90
Ile	Ser	Phe	Gly	Leu	Ser	Asp	Leu	Tyr	Gly	Asp	Asn	Arg	Val	His	95	100	105
Glu	Phe	Thr	Gly	Thr	Asp	Gly	Pro	Ser	Gly	Phe	Gly	Phe	Glu	Leu	110	115	120
Thr	Phe	Arg	Leu	Lys	Arg	Glu	Thr	Gly	Glu	Ser	Ala	Pro	Pro	Thr	125	130	135
Trp	Pro	Ala	Glu	Leu	Met	Gln	Gly	Leu	Ala	Arg	Tyr	Val	Phe	Gln	140	145	150
Ser	Glu	Asn	Thr	Phe	Cys	Ser	Gly	Asp	His	Val	Ser	Trp	His	Ser	155	160	165
Pro	Leu	Asp	Asn	Ser	Glu	Ser	Arg	Ile	Gln	His	Met	Leu	Leu	Thr	170	175	180
Glu	Asp	Pro	Gln	Met	Gln	Pro	Val	Gln	Thr	Pro	Phe	Gly	Val	Val	185	190	195
Thr	Phe	Leu	Gln	Ile	Val	Gly	Val	Cys	Thr	Glu	Glu	Leu	His	Ser	200	205	210
Ala	Gln	Gln	Trp	Asn	Gly	Gln	Gly	Ile	Leu	Glu	Leu	Leu	Arg	Thr	215	220	225
Val	Pro	Ile	Ala	Gly	Gly	Pro	Trp	Leu	Ile	Thr	Asp	Met	Arg	Arg	230	235	240
Gly	Glu	Thr	Ile	Phe	Glu	Ile	Asp	Pro	His	Leu	Gln	Glu	Arg	Val	245	250	255
Asp	Lys	Gly	Ile	Glu	Thr	Asp	Gly	Ser	Asn	Leu	Ser	Gly	Val	Ser	260	265	270
Ala	Lys	Cys	Ala	Trp	Asp	Asp	Leu	Ser	Arg	Pro	Pro	Glu	Asp	Asp	275	280	285
Glu	Asp	Ser	Arg	Ser	Ile	Cys	Ile	Gly	Thr	Gln	Pro	Arg	Arg	Leu	290	295	300
Ser	Gly	Lys	Asp	Thr	Glu	Gln	Ile	Arg	Glu	Thr	Leu	Arg	Arg	Gly	305	310	315
Leu	Glu	Ile	Asn	Ser	Lys	Pro	Val	Leu	Pro	Pro	Ile	Asn	Pro	Gln	320	325	330

Arg	Gln	Asn	Gly	Leu	Ala	His	Asp	Arg	Ala	Pro	Ser	Arg	Lys	Asp	335	340	345
Ser	Leu	Glu	Ser	Asp	Ser	Ser	Thr	Ala	Ile	Ile	Pro	His	Glu	Leu	350	355	360
Ile	Arg	Thr	Arg	Gln	Leu	Glu	Ser	Val	His	Leu	Lys	Phe	Asn	Gln	365	370	375
Glu	Ser	Gly	Ala	Leu	Ile	Pro	Leu	Cys	Leu	Arg	Gly	Arg	Leu	Leu	380	385	390
His	Gly	Arg	His	Phe	Thr	Tyr	Lys	Ser	Ile	Thr	Gly	Asp	Met	Ala	395	400	405
Ile	Thr	Phe	Val	Ser	Thr	Gly	Val	Glu	Gly	Ala	Phe	Ala	Thr	Glu	410	415	420
Glu	His	Pro	Tyr	Ala	Ala	His	Gly	Pro	Trp	Leu	Gln	Leu			425	430	

<210> 3

<211> 346

<212> DNA

<213> Artificial Sequence

<220>

<223> consensus DNA used to isolate DNA 33454

<220>

<221> unsure

<222> 8, 28, 39, 54-55, 65, 68, 74, 80, 90, 125, 130

<223> unknown base

<400> 3

ggactgcntg ccatagcggg ttccccgntc ccaccgcgnc cccggcccat 50

gccnnactgc ccccnegnc ttancatctn tctttccan gggactgcac 100

gccatctacg gagagtgcg cgcntttan ccttaccagc cgaaccgcgt 150

ccagggttacc gctatcgta agtactgggt ggggtggcca gacccttgg 200

actatgtag catgtacagg aatgtgggga gcccttctgc taacatcccc 250

gagcactggc actacatcag cttcggcctg agtgatctct atggtgacaa 300

cagagtccat gaagtttaca ggaacagatg gacctagtgg ttttgt 346

<210> 4

<211> 468

<212> PRT

<213> Drosophila Melanogaster

<400> 4

Met	Ala	Glu	Ala	Asn	Leu	Asp	Lys	Lys	Pro	Glu	Val	Lys	Pro	Pro	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Pro Gly Leu Lys	Ala	Ile Ile Asp His	Leu Gly Gln Val Tyr	Pro
	20		25	30
Asn Gln Pro Asn	Pro	Leu Gln Val Thr	Thr Leu Leu Lys Tyr	Trp
	35		40	45
Leu Gly Gly Gln	Asp	Pro Leu Asp Tyr	Ile Ser Met Tyr Lys	Phe
	50		55	60
Pro Gly Asp Val	Asp	Arg Asn Val Pro	Pro His Trp His Tyr	Ile
	65		70	75
Ser Phe Gly Leu	Ser	Asp Leu His Gly	Asp Glu Arg Val His	Leu
	80		85	90
Arg Glu Glu Gly	Val	Thr Arg Ser Gly	Met Gly Phe Glu Leu	Thr
	95		100	105
Phe Arg Leu Ala	Lys	Thr Glu Ile Glu	Leu Lys Gln Gln Ile	Glu
	110		115	120
Asn Pro Glu Lys	Pro	Gln Arg Ala Pro	Thr Trp Pro Ala Asn	Leu
	125		130	135
Leu Gln Ala Ile	Gly	Arg Tyr Cys Phe	Gln Thr Gly Asn Gly	Leu
	140		145	150
Cys Phe Gly Asp	Asn	Ile Pro Trp Arg	Lys Ser Leu Asp Gly	Ser
	155		160	165
Thr Thr Ser Lys	Leu	Gln Asn Leu Leu	Val Ala Gln Asp Pro	Gln
	170		175	180
Leu Gly Cys Ile	Asp	Thr Pro Thr Gly	Thr Val Asp Phe Cys	Gln
	185		190	195
Ile Val Gly Val	Phe	Asp Asp Glu Leu	Glu Gln Ala Ser Arg	Trp
	200		205	210
Asn Gly Arg Gly	Val	Leu Asn Phe Leu	Arg Gln Asp Met Gln	Thr
	215		220	225
Gly Gly Asp Trp	Leu	Val Thr Asn Met	Asp Arg Gln Met Ser	Val
	230		235	240
Phe Glu Leu Phe	Pro	Glu Thr Leu Leu	Asn Leu Gln Asp Asp	Leu
	245		250	255
Glu Lys Gln Gly	Ser	Asp Leu Ala Gly	Val Asn Ala Asp Phe	Ser
	260		265	270
Phe Arg Glu Leu	Lys	Pro Thr Lys Glu	Val Lys Glu Glu Val	Asp
	275		280	285
Phe Gln Ala Leu	Ser	Glu Lys Cys Ala	Asn Asp Glu Asn Asn	Arg
	290		295	300
Gln Leu Thr Asp	Thr	Gln Met Lys Arg	Glu Glu Pro Ser Phe	Pro
	305		310	315

Gln	Ser	Met	Ser	Met	Ser	Ser	Asn	Ser	Leu	His	Lys	Ser	Cys	Pro	
				320					325					330	
Leu	Asp	Phe	Gln	Ala	Gln	Ala	Pro	Asn	Cys	Ile	Ser	Leu	Asp	Gly	
				335					340					345	
Ile	Glu	Ile	Thr	Leu	Ala	Pro	Gly	Val	Ala	Lys	Tyr	Leu	Leu	Leu	
				350					355					360	
Ala	Ile	Lys	Asp	Arg	Ile	Arg	His	Gly	Arg	His	Phe	Thr	Phe	Lys	
				365					370					375	
Ala	Gln	His	Leu	Ala	Leu	Thr	Leu	Val	Ala	Glu	Ser	Val	Thr	Gly	
				380					385					390	
Ser	Ala	Val	Thr	Val	Asn	Glu	Pro	Tyr	Gly	Val	Leu	Gly	Tyr	Trp	
				395					400					405	
Ile	Gln	Val	Leu	Ile	Pro	Asp	Glu	Leu	Val	Pro	Arg	Leu	Met	Glu	
				410					415					420	
Asp	Phe	Cys	Ser	Ala	Gly	Leu	Asp	Glu	Lys	Cys	Glu	Pro	Lys	Glu	
				425					430					435	
Arg	Leu	Glu	Leu	Glu	Trp	Pro	Asp	Lys	Asn	Leu	Lys	Leu	Ile	Ile	
				440					445					450	
Asp	Gln	Pro	Glu	Pro	Val	Leu	Pro	Met	Ser	Leu	Asp	Ala	Ala	Pro	
				455					460					465	

Leu Lys Met

<210> 5

<211> 275

<212> DNA

<213> Mus musculus

<400> 5

gagagtgtcg ccgcctctac cctgaccagc cgaacccgct ccaggttacc 50

gctatcgtea agtactgggtt ggggtggccg gaccccttgg actatggttag 100

catgtacagg aacatgggga gtccttctgc caacatccct gagcactggc 150

actacatcag ctttggcctg agtgatctct atggtgacaa cagagtccat 200

gagtttacag gaacagacgg accaagtgga tttggctttg agttgacgtt 250

tcgtctgaag agagaaactg gggag 275

<210> 6

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> forward PCR cloning primer

<400> 6  
 cagccgaacc cgctccaggt tac 23

<210> 7  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> reverse PCR cloning primer

<400> 7  
 catggactct gttgtcacca tagag 25

<210> 8  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> hybridization probe

<400> 8  
 gagcactggc actacatcag ctttggcctg agtgatctct 40

<210> 9  
 <211> 441  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> hSu(fu) epitope flag protein

<400> 9  
 Met Ala Glu Leu Arg Pro Ser Gly Ala Pro Gly Pro Thr Ala Pro  
 1 5 10 15  
 Pro Ala Pro Gly Pro Thr Ala Pro Pro Ala Phe Ala Ser Leu Phe  
 20 25 30  
 Pro Pro Gly Leu His Ala Ile Tyr Gly Glu Cys Arg Arg Leu Tyr  
 35 40 45  
 Pro Asp Gln Pro Asn Pro Leu Gln Val Thr Ala Ile Val Lys Tyr  
 50 55 60  
 Trp Leu Gly Gly Pro Asp Pro Leu Asp Tyr Val Ser Met Tyr Arg  
 65 70 75  
 Asn Val Gly Ser Pro Ser Ala Asn Ile Pro Glu His Trp His Tyr  
 80 85 90  
 Ile Ser Phe Gly Leu Ser Asp Leu Tyr Gly Asp Asn Arg Val His  
 95 100 105  
 Glu Phe Thr Gly Thr Asp Gly Pro Ser Gly Phe Gly Phe Glu Leu  
 110 115 120

Thr	Phe	Arg	Leu	Lys	Arg	Glu	Thr	Gly	Glu	Ser	Ala	Pro	Pro	Thr	
				125					130					135	
Trp	Pro	Ala	Glu	Leu	Met	Gln	Gly	Leu	Ala	Arg	Tyr	Val	Phe	Gln	
				140					145					150	
Ser	Glu	Asn	Thr	Phe	Cys	Ser	Gly	Asp	His	Val	Ser	Trp	His	Ser	
				155					160					165	
Pro	Leu	Asp	Asn	Ser	Glu	Ser	Arg	Ile	Gln	His	Met	Leu	Leu	Thr	
				170					175					180	
Glu	Asp	Pro	Gln	Met	Gln	Pro	Val	Gln	Thr	Pro	Phe	Gly	Val	Val	
				185					190					195	
Thr	Phe	Leu	Gln	Ile	Val	Gly	Val	Cys	Thr	Glu	Glu	Leu	His	Ser	
				200					205					210	
Ala	Gln	Gln	Trp	Asn	Gly	Gln	Gly	Ile	Leu	Glu	Leu	Leu	Arg	Thr	
				215					220					225	
Val	Pro	Ile	Ala	Gly	Gly	Pro	Trp	Leu	Ile	Thr	Asp	Met	Arg	Arg	
				230					235					240	
Gly	Glu	Thr	Ile	Phe	Glu	Ile	Asp	Pro	His	Leu	Gln	Glu	Arg	Val	
				245					250					255	
Asp	Lys	Gly	Ile	Glu	Thr	Asp	Gly	Ser	Asn	Leu	Ser	Gly	Val	Ser	
				260					265					270	
Ala	Lys	Cys	Ala	Trp	Asp	Asp	Leu	Ser	Arg	Pro	Pro	Glu	Asp	Asp	
				275					280					285	
Glu	Asp	Ser	Arg	Ser	Ile	Cys	Ile	Gly	Thr	Gln	Pro	Arg	Arg	Leu	
				290					295					300	
Ser	Gly	Lys	Asp	Thr	Glu	Gln	Ile	Arg	Glu	Thr	Leu	Arg	Arg	Gly	
				305					310					315	
Leu	Glu	Ile	Asn	Ser	Lys	Pro	Val	Leu	Pro	Pro	Ile	Asn	Pro	Gln	
				320					325					330	
Arg	Gln	Asn	Gly	Leu	Ala	His	Asp	Arg	Ala	Pro	Ser	Arg	Lys	Asp	
				335					340					345	
Ser	Leu	Glu	Ser	Asp	Ser	Ser	Thr	Ala	Ile	Ile	Pro	His	Glu	Leu	
				350					355					360	
Ile	Arg	Thr	Arg	Gln	Leu	Glu	Ser	Val	His	Leu	Lys	Phe	Asn	Gln	
				365					370					375	
Glu	Ser	Gly	Ala	Leu	Ile	Pro	Leu	Cys	Leu	Arg	Gly	Arg	Leu	Leu	
				380					385					390	
His	Gly	Arg	His	Phe	Thr	Tyr	Lys	Ser	Ile	Thr	Gly	Asp	Met	Ala	
				395					400					405	
Ile	Thr	Phe	Val	Ser	Thr	Gly	Val	Glu	Gly	Ala	Phe	Ala	Thr	Glu	
				410					415					420	



Glu His Pro Tyr Ala Ala His Gly Pro Trp Leu Gln Leu Asp Tyr  
 425 430 435

Lys Asp Asp Asp Asp Lys  
 440

<210> 10  
 <211> 658  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> hSu(fu)-GST protein

<400> 10  
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln  
 1 5 10 15  
 Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu  
 20 25 30  
 His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys  
 35 40 45  
 Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp  
 50 55 60  
 Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile  
 65 70 75  
 Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala  
 80 85 90  
 Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly  
 95 100 105  
 Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val  
 110 115 120  
 Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp  
 125 130 135  
 Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His  
 140 145 150  
 Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met  
 155 160 165  
 Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys  
 170 175 180  
 Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser  
 185 190 195  
 Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe  
 200 205 210  
 Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly  
 215 220 225

Ser Ala Glu Leu Arg	Pro Ser Gly Ala	Pro Gly Pro Thr Ala	Pro
230		235	240
Pro Ala Pro Gly Pro	Thr Ala Pro Pro	Ala Phe Ala Ser Leu	Phe
245		250	255
Pro Pro Gly Leu His	Ala Ile Tyr Gly	Glu Cys Arg Arg Leu	Tyr
260		265	270
Pro Asp Gln Pro Asn	Pro Leu Gln Val	Thr Ala Ile Val Lys	Tyr
275		280	285
Trp Leu Gly Gly Pro	Asp Pro Leu Asp	Tyr Val Ser Met Tyr	Arg
290		295	300
Asn Val Gly Ser Pro	Ser Ala Asn Ile	Pro Glu His Trp His	Tyr
305		310	315
Ile Ser Phe Gly Leu	Ser Asp Leu Tyr	Gly Asp Asn Arg Val	His
320		325	330
Glu Phe Thr Gly Thr	Asp Gly Pro Ser	Gly Phe Gly Phe Glu	Leu
335		340	345
Thr Phe Arg Leu Lys	Arg Glu Thr Gly	Glu Ser Ala Pro Pro	Thr
350		355	360
Trp Pro Ala Glu Leu	Met Gln Gly Leu	Ala Arg Tyr Val Phe	Gln
365		370	375
Ser Glu Asn Thr Phe	Cys Ser Gly Asp	His Val Ser Trp His	Ser
380		385	390
Pro Leu Asp Asn Ser	Glu Ser Arg Ile	Gln His Met Leu Leu	Thr
395		400	405
Glu Asp Pro Gln Met	Gln Pro Val Gln	Thr Pro Phe Gly Val	Val
410		415	420
Thr Phe Leu Gln Ile	Val Gly Val Cys	Thr Glu Glu Leu His	Ser
425		430	435
Ala Gln Gln Trp Asn	Gly Gln Gly Ile	Leu Glu Leu Leu Arg	Thr
440		445	450
Val Pro Ile Ala Gly	Gly Pro Trp Leu	Ile Thr Asp Met Arg	Arg
455		460	465
Gly Glu Thr Ile Phe	Glu Ile Asp Pro	His Leu Gln Glu Arg	Val
470		475	480
Asp Lys Gly Ile Glu	Thr Asp Gly Ser	Asn Leu Ser Gly Val	Ser
485		490	495
Ala Lys Cys Ala Trp	Asp Asp Leu Ser	Arg Pro Pro Glu Asp	Asp
500		505	510
Glu Asp Ser Arg Ser	Ile Cys Ile Gly	Thr Gln Pro Arg Arg	Leu
515		520	525

Ser Gly Lys Asp	Thr Glu Gln Ile Arg	Glu Thr Leu Arg Arg Gly	530	535	540
Leu Glu Ile Asn	Ser Lys Pro Val Leu	Pro Pro Ile Asn Pro Gln	545	550	555
Arg Gln Asn Gly	Leu Ala His Asp Arg	Ala Pro Ser Arg Lys Asp	560	565	570
Ser Leu Glu Ser	Asp Ser Ser Thr Ala	Ile Ile Pro His Glu Leu	575	580	585
Ile Arg Thr Arg	Gln Leu Glu Ser Val	His Leu Lys Phe Asn Gln	590	595	600
Glu Ser Gly Ala	Leu Ile Pro Leu Cys	Leu Arg Gly Arg Leu Leu	605	610	615
His Gly Arg His	Phe Thr Tyr Lys Ser	Ile Thr Gly Asp Met Ala	620	625	630
Ile Thr Phe Val	Ser Thr Gly Val Glu	Gly Ala Phe Ala Thr Glu	635	640	645
Glu His Pro Tyr	Ala Ala His Gly Pro	Trp Leu Gln Leu	650	655	